

Features of Human Slit-1 predicted protein Co-ordinates refer to amino acid number.

Signal sequence:	7-24	
First amino-flanking sequence:	28-59	
First set of Leucine Rich Repeats:	60-179	(6 repeats)
First carboxy-flanking sequence:	180-276	
Second amino-flanking sequence:	277-308	
Second set of Leucine Rich Repeats:	309-434	(5 repeats)
Second carboxy-flanking sequence:	435-501	
Third amino-flanking sequence:	502-533	
Third set of Leucine Rich Repeats:	534-660	(5 repeats)
Third carboxy-flanking sequence:	661-722	
Fourth amino-flanking sequence:	723-754	
Fourth set of Leucine Rich Repeats:	755-855	(4 repeats)
Fourth carboxy-flanking sequence:	856-917	
First EGF repeat:	918-952	
Second EGF repeat:	953-993	
Third EGF repeat:	994-1031	
Fourth EGF repeat:	1032-1071	
Fifth EGF repeat:	1072-1109	
Spacer:	1110-1116	
Sixth EGF repeat:	1117-1154	
"99aa spacer":	1155-1329	
Seventh EGF repeat:	1330-1366	
Eighth EGF repeat:	1367-1404	
Ninth EGF repeat:	1405-1447	
Cysteine knot motif:	1448-1525	

Leucine rich repeats (LRRs) are predicted by comparison with known proteins and by the presence of the core sequence: xxxFxxLxxLxxLxLxxNxIxxL, where x is any amino acid. In slit proteins, the LRRs are flanked by conserved sequences referred to as the amino- and carboxy- flanking regions. These flanking regions are found in other known proteins, but only in a few instances are both the amino- and carboxy- flank regions present in a single protein. The amino flank region is defined by the consensus: CPxxCxC[1-6x]GxxVDCxxxGL[2-4x] α Pxx α Pxdttx where x is any amino acid, [x] represents a variable number of amino acids and α is a hydrophobic residue. Lower case indicates a residue is not highly conserved at a particular position. The carboxy flank region is defined by the consensus: P β C γ Cx α [1-5x]W α [14-26x]RCxxPxxxxxxxx α xx α xxxxF[1-3x]Cs[3-17x] where β is W or a hydrophobic residue, γ is D or N and α is a hydrophobic residue.

Epidermal growth factor (EGF) repeats are predicted by the consensus: CxxxxCxnxC[6-9x] α CxCxxG α GxxCxxxxxx.

The so called "99aa spacer" is actually ~200 amino acids in the *Drosophila* protein and 174 amino acids in Human Slit-1. This region shows homology to the G-loops of laminin A chains.

Cysteine knots are dimerisation domains defined by the presence of six cysteine residues between which disulphide bridges form. The only absolutely conserved residues are the six cysteines, and spacing between them is highly variable, apart from between cysteines 2 and 3, and 5 and 6: C[x]C[1-3x]GxC[x]C[x]CxC. The glycine between cysteines 2 and 3 is only present in a subset of cysteine knots. *Drosophila* slit and Human slit-1 both have an extra cysteine after cysteines 5 and 6: this may serve as an intermolecular bond.

Human Slit-1 gene displays the overall structure of the *Drosophila* gene, and amino acid conservation is found along the entire length of the protein (48% homology at the amino acid sequence excluding the signal sequence; see below). The Human gene has an extra LRR between LRR2 and LRR3 of the first set of LRRs; in the third set, the Human gene has an extra LRR between LRR3 and LRR4. The Human gene has two extra EGF repeats, on either side of the seventh EGF repeat in *Drosophila* slit.

Isolation of Human slit-1

Searching of the EST database revealed an EST, ab16g10.r1, with homology to the 99aa spacer region of *Drosophila* slit. This EST was used to probe a Human fetal brain library (Stratagene), and clones for Human slit-1 were isolated.

Amino acid identity between Drosophila Slit and Human Slit-1

First amino-flanking sequence:	53%	
First set of Leucine Rich Repeats:	52%	(54%, 67%, NA, 38%, 54%, 50%)
First carboxy-flanking sequence:	42%	
Second amino-flanking sequence:	50%	
Second set of Leucine Rich Repeats:	60%	(54%, 58%, 67%, 71%, 50%)
Second carboxy-flanking sequence:	62%	
Third amino-flanking sequence:	56%	
Third set of Leucine Rich Repeats:	49%	(46%, 46%, 42%, NA, 58%)
Third carboxy-flanking sequence:	36%	
Fourth amino-flanking sequence:	53%	
Fourth set of Leucine Rich Repeats:	48%	(25%, 58%, 46%, 63%)
Fourth carboxy-flanking sequence:	63%	
First EGF repeat:	34%	
Second EGF repeat:	46%	
Third EGF repeat:	46%	
Fourth EGF repeat:	35%	
Fifth EGF repeat:	47%	
Spacer:	22%	
Sixth EGF repeat:	40%	
"99aa spacer":	38%	
Seventh EGF repeat:	11%/NA	
Eighth EGF repeat:	44%	
Ninth EGF repeat:	29%/NA	
Cysteine knot motif:	34%	

NA: not applicable due to absence of homologous repeat.
Figures for individual LRRs are shown in brackets.

TABLE 3

Alignment of

Slit sequences

1	M A A P S R T T L M P P P F R L Q L R L - L I L P I L L L L R H D A V H A E P Y	D-Slit
1	M R G V G W Q - - - - - M L S L S L G L V L A I L - - - - -	H-Slit1
40	S G G F G S S A V S S G G L G S V G I H I P G G G V G V I T E A R C P R V C S C	D-Slit
21	- - - - - - - - - - - - - - - - - N K V A P Q A C P A Q C S C	H-Slit1
80	T G L N V D C S H R G L T S V P R K I S A D V E R L E L Q G N N I T V I Y E T D	D-Slit
35	S G S T V D C H G L A I R S V P R N I P R N T E R L D L N G N N I T R I T K T D	H-Slit1
120	F Q R L T K L R M L Q L T D N Q I H T I E R N S F Q D L V S L E R L - - - - -	D-Slit
75	F A G L R H L R V L Q L M E N K I S T I E R G A F Q D L K E L E R L R L N R N H	H-Slit1
1	H L R V L Q L M E N R I S T I E R G A F Q D L K E L E R L R L N R N N	M-Slit1
154	- - - - - - - - - - - - - D I S N N V I T T V G R R V F K G A Q S L R	D-Slit
115	L Q L F P E L L F L G T A K L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	H-Slit1
36	L O L F P E L L F L G T A R L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	M-Slit1
176	S L Q L D N N Q I T C L D E H A F K G L V E L E I L T L N N N N L T S L P H N I	D-Slit
155	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	H-Slit1
76	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	M-Slit1
216	F G G L G R L R A L R L S D N P F A C D C H L S W L S R F L R S A T R L A P Y T	D-Slit
195	F N H M P K L R T F R L H S N N L Y C D C H L A W L S D W L R K R P R V G L Y T	H-Slit1
116	F N H M P K L R T F R L H S N N L Y C	M-Slit1
236	R C Q S P S Q L K G Q N V A D L H D Q E F K C S G L T E - H A P M - - - E C G A	D-Slit
235	Q C M G P S H L R G H N V A E V Q R E F V C S D E E E G H Q S F M A P S C S V	H-Slit1
292	E N S C P H P C R C A D G I V D C R E K S L T S V P V T L P D D T T D V R L E Q	D-Slit
275	L H - C P A A C T C S N N I V D C R G K G L T E I P T N L P E T I T E I R L E Q	H-Slit1
10	S P C T C S N N I V D C R G K G L M E I P A N L P E G I V E I R L E Q	H-Slit2
332	N F I T E L P P K S F S S F R R L R R I D L S N N N I S R I A H D A L S G L K Q	D-Slit
314	N T I K V I P P G A F S P Y K K L R R I D L S N N Q I S E L A P D A F Q G L R S	H-Slit1
36	N S I K A I P A G A F T Q Y K K L K R I D I S K N Q I S D I A P D A F O G L K S	H-Slit2
372	L T T L V L Y G N K I K D L P S G V F K G L G S L R L L L L N A N E I S C I R K	D-Slit
354	L N S L V L Y G N K I T E L P K S L F E G L F S L Q L L L L N A N K I N C L R V	H-Slit1
76	L T S L V L Y G N K I T E I A K G L F D G L V S L O L L L L	H-Slit2
1	- R	CE-Slit
412	D A F R D L H S L S L L S L Y D N N I Q S L A N G T F D A M K S M K T V H L A K	D-Slit1
394	D A F Q D L H N L N L L S L Y D N K L Q T I A K G T F S P L R A I Q T M H L A Q	H-Slit1
2	N P X I C D C N L Q W L A Q I N L Q K N I E T S G A R C E Q P K R L R K K K F A	CE-Slit
452	N P F I C D C N L R W L A D Y L H K N P I E T S G A R C E S P K R M H R R R I E	D-Slit
434	N P F I C D C H L K W L A D Y L H T N P I E T S G A R C T S P R R L A N K R I G	H-Slit1
42	T L P P N K F K C K G S E S F V S M Y A D S C F I D S I C P T Q C D C Y G T T V	CE-Slit
492	S L R E E K F K C S - W G E L R M K L S G E C R M D S D C P A M C H C E G T T V	D-Slit
474	Q I K S K K F R C S G T E D Y R S K L S G D C F A D L A C P E K C R C E G T T V	H-Slit1

82	DCNKRG	LNTIPT	STPR	FATQ	LLLS	SGNN	ISTV	DLNS	NIHV	L	CE-Slit				
531	DCTGR	RRLKE	IPRD	IPLHT	TELL	LLND	NELG	RIS	SSD	GLFGR	L	D-Slit			
514	DCSNQ	KLNK	IPEH	IPQY	TAE	LRLN	NNNE	FTV	LEAT	GIFK	KL	H-Slit1			
122	ENLEX	LDLS	NNH	ITF	IND	KSF	EKLS	KLREL	XLND			CE-Slit			
571	PHLV	KLEL	KRN	QLTG	IEPN	AFEG	ASHI	QELQ	LG	ENK	IK	KEI	D-Slit		
554	PQLR	KINF	SNNK	ITDI	EEGA	AFEG	ASGV	NEIL	LLTS	SNRL	EN	V	H-Slit1		
1					EGAF	NGAA	ASV	QELM	LTG	NQLE	TV		H-Slit2		
611	SNKMF	-	-	-	-	-	-	-	-	-	-	-	D-Slit		
594	QH	KMF	KG	-	LES	LK	TLML	RSNR	ITCV	GNDS	FI	GLSS	SVRL	L	H-Slit1
24	HGR	GFR	GG	LSG	LK	TLML	RSNL	IGCV	SNDT	FA	GLSS	SVRL	L		H-Slit2
626	LYDN	QISC	VMP	PGS	FEL	NSLT	SLNLA	SNPF	NCNCH	LAW	-	F		D-Slit	
633	LYDN	QITT	VAP	GAFD	TLHS	SLST	LNLL	ANPF	NCNC	YLAW	-	L		H-Slit1	
64	LYDN	RITT	ITP	GAF	TLV	SLST	INLL	SNPF	NCNCH	L	GAGL			H-Slit2	
665	AEC	VRRK	SLNG	GAAR	C	GAP	SKVR	DVQ	IKDL	PHSE	FKCS	SS	E	D-Slit	
672	GEWL	RKKR	IVT	GNPR	CQK	PY	FLKE	IP	IQDV	AIQD	FTCD	DD	G	H-Slit1	
104	GKWL	RKR	IVS	GNPR	CQK	PF	FLKE	IP	IQGV	GH	PGI			H-Slit2	
1															
705	NSE	-	GCL	GDGY	CPPS	CTCT	GTVA	ACSR	NQLKE	IPRG	IPAE			CE-Slit	
712	HDD	NSC	SPLS	RCPTE	CTCL	DTV	VRCS	NKGL	KVLP	KGIP	PRD			D-Slit	
16	TE	ELYLD	ANY	INE	IPAH	DI	NRL	LYSL	TKLD	LSHN	RLIS	LEN		H-Slit1	
744	TSE	LYLE	SNE	IEQ	IHYE	RI	HLR	SLTR	RLD	LSNN	QIT	ILSN		CE-Slit	
752	VTE	LYLD	G	NQFT	LV	PKF	-	LSNY	KH	LT	LID	LSNN	RIST	D-Slit	
56	NT	FSNL	TR	LST	LIIS	YNKL	RCLQ	PLAF	NG	LNAL	RLIS	LSLHG		H-Slit1	
784	YTF	ANL	TKL	LST	LIIS	YNKL	QCLQ	RHAL	SGLN	NNLR	VVSL	LSLHG		CE-Slit	
791	QSF	SNMT	Q	LLT	LIIS	YNRL	RCIP	PRTF	DGLK	SLRL	LSLHG			D-Slit	
96	ND	ISF	LPOS	AFS	NLT	SI	THIA	VGS	NSLY	CDCN	MAW	F	SKWI	H-Slit1	
824	NR	ISM	LPEG	SFED	LKSL	THIA	LGS	NPLY	CDC	GLK	WFSD	W	I	CE-Slit	
831	ND	ISV	VPEG	AFND	LSA	LSHL	AIGA	NPLY	CDCN	HQW	LS	SDW	V	D-Slit	
436	KSK	FIE	AGI	ARCE	EYP	NTV	SNQ	LLLT	TAQ	PYQ	FTCD	SKV	PTK	H-Slit1	
864	KLD	YVE	PGI	ARCA	EPE	QM	KDK	LI	LS	TPSS	SFV	CRGR	VRND	CE-Slit	
871	KSE	YKE	PGI	ARCA	GPG	EM	ADK	LLLT	TPSK	KKFT	CQGP	V	DVN	D-Slit	
176	LAT	KCDL	C	LN	SPCK	NNAI	CET	TSSR	KYTC	NC	TPGF	YGV	HC	H-Slit1	
904	ILA	KCN	AC	FEQ	PCQ	Q	AQC	VALP	QREY	QC	CPGY	HGK	HC	CE-Slit	
911	ILA	KCN	PC	LSN	PC	KND	GTC	NSD	PVDF	YRCT	CPY	GFK	QDC	D-Slit	
216	ENQ	IDAC	YGS	PC	LNN	NATCK	V	-	AQ	AGR	FN	CYCN	KGF	EGDY	H-Slit1
944	EFM	IDAC	YGN	PC	RNN	NATCT	VLE	-	EG	RFS	CQ	CAPG	YTGA	CE-Slit	
951	DVP	I	HAC	IS	NPC	KHGG	TCHL	KEGE	EDGF	WC	ICAD	G	FEGEN	D-Slit	
254	CEK	NIDDC	V	-	NSK	CENG	G	GK	CVDL	V	RFC	SEEL	KNF	QSF	H-Slit1
982	CET	NIDDC	LGE	IK	Q	NNATC	ID	-	-	-	-	-	-	GVE	CE-Slit
991	CEV	NVDDC	-	EDND	CENN	S	TCVD	-	-	-	-	-	-	GIN	D-Slit

293 SYRCD CPM EYE GKHCED KLEYCTKK LNPCEN NGKCIP IN G CE-Slit
1007 SYKCEC QPGFS GEFCDTK IQFCSP EFNPCAN GA KCM D H FT D-Slit
1015 NYTCLCPPEYT GELCEEK LDFCAQDLNPCQHDS KCILTPK H-Slit1
1 DPLPV M-Slit2

333 SYSCMCSPGFTGN NCE T NIDDCKNVE CQNGGS SCVDGILSY CE-Slit
1047 HYS CDCQAGFHGTNCTDN IDDCQNHMCONGGT CVDGIN DY D-Slit
1055 GFKC DCTPGYVGEHC D IDFD DDCQDNKCKNGA HCTDAVNGY H-Slit1
1 NNDDCVGHKCRHGAQCVDDEVNGY M-Slit1
1 WPRCECMPGYAGDNCSENQDDCRDHR CQNGAQC MDEVNSY H-Slit2
6 HHRCECHLGYTGDNCS ENODDC KDHKCQNGAQCVDDEVNSY M-Slit2

373 DCLCRPGYAGQYCEIPPM MDHEYQKTDACQQSACGQG-EC CE-Slit
1087 QCRCPDDYT GK YCE GHNM ISM MY PQTSPCQNH ECKHGV-C D-Slit
1095 TCICPEGYSGLFCE FSP--PMVLPRTSPCDNFDCQNGAQC H-Slit1
24 TCICPQGFSGLFCE HPP--PMVL LQTSPCDQYECQNGAQC M-Slit1
41 SCLCAEGYSGLCEIPP--HLPAPK-SPCEGTECQNGANC H-Slit2
46 ACLCV EGYSGQLCEIPP--APR-SSCEGTECQNGANC M-Slit2

412 VASQN-S SDF TCKCHEGFS GSPSCDRQMSVGFKNPGAYLAL CE-Slit
1126 FQPNAGGSDYL CRCHPGYT GKWCEYLTSISFVHNNSFVEL D-Slit
1133 IVRINEP---ICQCLPGYQGEKCEKLVSVNFINKESYLQI H-Slit1
62 IVVQQEP---TCRCPPGFAGPRCEKLI TVNFV G KDSYVEL M-Slit1
78 VDQGNRP---VCQCLPGFGGPECEKLLSVNFVDRD TYLQF H-Slit2
80 VDQGSRP---VCQCLPGFGGPECEKLLSVNFVDRD TYLQF M-Slit2

451 DPLAS--DGTITMTLRTTSKIGILLYY GDDH FVSAELYD G CE-Slit
1166 EPLRTRPEANVTIVFS SAEQNGILMYD GQDAHLA VELFNG D-Slit
1170 PSAKVRPQT NITLOIA TDEDSGILLYK GDK KDHIAVELYRG H-Slit1
99 ASAKVR M-Slit1
115 TDLQNW XRXNITLQVF FTAEDNGILLYNGG GNDHIAV XLYXG H-Slit2
117 TDLQNWPRANITLOVSTAEDNGILLYNGDNDHIAVELY M-Slit2

489 RVKL VYYIGNFPASH MYSSVKVNDGLPHRISIRTSERKCF CE-Slit
1206 RIRVSYDVGNHPVSTHYSFEMVADGKYH AVELLA I KKNFT D-Slit
1210 RVRAS YDTGSHPASAIYSVETINDGNFHI VELLALDQSLS H-Slit1
155 HVRFSY H-Slit2

529 LQIDKNPVQIVENS SGKSDQLITKGKEMLYIGGLPIEKSQD CE-Slit
1246 LRVDRGLARS IINEG SNDYL--KLTT P MFLGGLPVDP AQQ D-Slit
1250 LSV DGGNFK IITNL SKQSTL--NFDSPLYVGGMP PGKSNVA H-Slit1
1 ILDVA M-Slit1

569 AKRRFHVKNSESLKGC ISSITINEVPINLQQALENVNTEQ CE-Slit
1284 AYKNWQIRNLTSFKGCMKEVWINHKLVD FGN AQRRQKITP D-Slit
1288 SLRQAPGQNGTSF HGCIRNLYINSELQDFQKVPMQTGILP H-Slit1
6 SLRQAPGE NGTSF HGCIRNLYINSELQDFRKM PMOTGILP M-Slit1

609 SC-----SATVNF----- CE-Slit
1324 G CAL-----LEGEQQEEEDDEQDFMDE-----TPHIKEEP D-Slit
1328 GCEPCHKKVCAHGT CQPS SQA GFTCECQEGWMGPLCDQRT H-Slit1
46 GCEPCHKKVCAHGC CQPS SQS GFTCECEEGWMGPLCDQRT M-Slit1

TABLE 4

Alignment of Drosophila Slit and Human Slit-1

1	M A A P S R T T L M P P P F R L Q L R L - L I L P I L L L L R H D A V H A E P Y	D-Slit
1	M R G V G W Q - - - - - M L S L S L G L V L A I L - - - - -	H-Slit1
40	S G G F G S S A V S S G G L G S V G I H I P G G V G V I T E A R C P R V C S C	D-Slit
21	- - - - - - - - - - - - - - - - - N K V A P Q A C P A Q C S C	H-Slit1
80	T G L N V D C S H R G L T S V P R K I S A D V E R L E L Q G N N L T V I Y E T D	D-Slit
35	S G S T V D C H G L A L R S V P R N I P R N T E R L D L N G N N I T R I T K T D	H-Slit1
120	F Q R L T K L R M L Q L T D N Q I H T I E R N S F Q D L V S L E R L - - - - -	D-Slit
75	F A G L R H L R V L Q L M E N K I S T I E R G A F Q D L K E L E R L R L N R N H	H-Slit1
154	- - - - - - - - - - - - - - - - - D I S N N V I T T V G R R V F K G A Q S L R	D-Slit
115	L Q L F P E L L F L G T A K L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	H-Slit1
176	S L Q L D N N Q I T C L D E H A F K G L V E L E I L T L N N N N L T S L P H N I	D-Slit
155	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	H-Slit1
216	F G G L G R L R A L R L S D N P F A C D C H L S W L S R F L R S A T R L A P Y T	D-Slit
195	F N H M P K L R T F R L H S N N L Y C D C H L A W L S D W L R K R P R V G L Y T	H-Slit1
256	R C Q S P S Q L K G Q N V A D L H D Q E F K C S G L T E - H A P M - - - E C G A	D-Slit
235	Q C M G P S H L R G H N V A E V Q K R E F V C S D E E E G H Q S F M A P S C S V	H-Slit1
292	E N S C P H P C R C A D G I V D C R E K S L T S V P V T L P D D T T D V R L E Q	D-Slit
275	L H - C P A A C T C S N N I V D C R G H G L T E I P T N L P E T I T E I R L E Q	H-Slit1
332	N F I T E L P P K S F S S F R R L R R I D L S N N N I S R I A H D A L S G L K Q	D-Slit
314	N T I K V I P P G A F S P Y K K L R R I D L S N N Q I S E L A P D A F Q G L R S	H-Slit1
372	L T T L V L Y G N K I K D L P S G V F K G L G S L R L L L L N A N E I S C I R K	D-Slit
354	L N S L V L Y G N K I T E L P K S L F E G L F S L Q L L L L N A N K I N C L R V	H-Slit1
412	D A F R D L H S L S L L S L Y D N N I Q S L A N G T F D A M K S M K T V H L A K	D-Slit
394	D A F Q D L H N I N L L S L Y D N K L Q T I A K G T F S P L R A I Q T M H L A Q	H-Slit1
452	N P F I C D C N L R W L A D Y L H K N P I E T S G A R C E S P K R M H R R R I E	D-Slit
434	N P F I C D C H L K W L A D Y L H T N P I E T S G A R C T S P R R L A N K R I G	H-Slit1
492	S L R E E K F K C S - W G E L R M K L S G E C R M D S D C P A M C H C E G T T V	D-Slit
474	Q I K S K K F K C S G T E D Y R S K L S G D C F A D L A C P E K C R C E G T T V	H-Slit1
531	D C T G R R L K E I P R D I P L H T T E L L L N D N E L G R I S S D G L F G R L	D-Slit
514	D C S N Q K L N K I P E H I P Q Y T A E L R L N N N E F T V L E A T G I F K K L	H-Slit1
571	P H L V K L E L K R N Q L T G I E P N A F E G A S H I Q E L Q L G E N K I K E I	D-Slit
554	P Q L R K I N F S N N K I T D I E E G A F E G A S G V N E I L L T S N R L E N V	H-Slit1
611	S N K M F L G L H Q L K T L - - - - - - - - - - - - - - - - - N L	D-Slit
594	Q H K M F K G L E S L K T L M L R S N R I T C V G N D S F I G L S S V R L L S L	H-Slit1
627	Y D N Q I S C V M P G S F E H L N S L T S L N L A S N P F N C N C H L A W F A E	D-Slit
634	Y D N Q I T T V A P G A F D T L H S L S T L N L L A N P F N C N C Y L A W L G E	H-Slit1

667 C V R K K S L N G G A A R Q A P S K V R D V Q I K D L P H S K C S S E N S D-Slit
674 W L R K K R I V T G N P R C Q K P Y F L K E I P I Q D V A I Q D T C D D G N D H-Slit1

707 E - G C L G D G Y C P P S C T C T G T V V A C S R N Q L K E I P R G I P A E T S D-Slit
714 D N S C S P L S R C P T E C T C L D T V V R C S N K G L K V L P K G I P R D V T H-Slit1

746 E L Y L E S N E I E Q I H Y E R I R H L R S L T R L D L S N N Q I T I L S N Y T D-Slit
754 E L Y L D G N Q F T L V P K E - L S N Y K H L T L I D L S N N R I S T L S N Q S H-Slit1

786 F A N L T K L S T L I I S Y N K L Q C L Q R H A L S G L N N L R V V S L H G N R D-Slit
793 F S N M T Q L L T L I L S Y N R L R C I P P R T F D G L K S L R L L S L H G N D H-Slit1

826 I S M L P E G S F E D L K S L T H I A L G S N P L Y C D C G L K W F S D W I K L D-Slit
833 I S V V P E G A F N D L S A L S H L A I G A N P L Y C D C N M Q L S D W V K S H-Slit1

866 D Y V E P G I A R C A E P E Q M K D K L I L S T P S S S F V C R G R V R N D I L D-Slit
873 E Y K E P G I A R C A G P G E H A D K L L L T P S K K E T C Q G P V D V N I L H-Slit1

906 A K C N A C F E Q P C Q N Q A Q C V A L P Q R E Y Q C L C Q P G Y H G K H C E F D-Slit
913 A K C N P C L S N P C K N D G T C N S D P V D F Y R C T C P Y G F K G Q D C D V H-Slit1

946 M I D A C Y G N P C R N N A T C T V L E - - E G R F S C Q C A P G Y T G A R C E D-Slit
953 P I H A C I S N P C K H G G T C H L K E G E E D G F W C I C A D G F E G E N C E H-Slit1

984 T H I D D C L G E I K C Q N H A T C I D G V E S Y K C E C Q P G F S G E F C D T D-Slit
993 V H V D D C - E D N D C E N H S T C V D G I N N Y T C L C P P E Y T G E L C E E H-Slit1

1024 K I Q F C S P E F H P C A N G A K C M D H F T H Y S C D C Q A G F H G T N C T D D-Slit
1032 K L D F C A Q D L N P C Q H D S K C I L T E K G F K C D C T P G Y V G E H C D I H-Slit1

1064 N I D D C Q N H M C Q N G G T C V D G I N D Y Q C R C P D D Y T G K Y C E G H N D-Slit
1072 D F D D C Q D N K C K N G A H C T D A Y H G Y T C I C P E G Y S G L F C E F S P H-Slit1

1104 M I S M M Y P Q T S P C Q N H E C K H G V - C F Q P N A Q G S D Y L C R C H P G D-Slit
1112 - - P M V L P R T S P C D H F D C Q N G A Q C I - - - V R I N E P I C Q C L P G H-Slit1

1143 Y T G K W C E Y L T S I S F V H N N S F V E L E P L R T R P E A N V T I V F S S D-Slit
1147 Y Q G E K C E K L V S V N F I N K E S Y L Q I P S A K V E P Q T H I T L Q I A T H-Slit1

1183 A E Q N G I L M Y D G Q D A H L A V E L F N G R I R V S Y D V G N H P V S T M Y D-Slit
1187 D E D S G I L L Y K G D K D H I A V E L Y R G R V R A S Y D T G S H P A S A I Y H-Slit1

1223 S F E M V A D G K Y H A V E L L A I K K N F T L R V D R G L A R S I I N E G S N D-Slit
1227 S V E T I N D G N F H I V E L L A L D Q S L S I S V D G G N P K I I T N L S K Q H-Slit1

1263 D Y L K L T T P M F L G G L P V D P A Q Q A Y K N W Q I R N L T S F K G C M K E D-Slit
1267 S T L N F D S P L Y V G G M P G K S N V A S L R Q A P G Q N G T S F H G C I R N H-Slit1

1303 V W I N H K L V D F G N A Q R Q Q K I T P G C A L - - - - L E G E Q Q E E E D D D-Slit
1307 L Y I N S E L Q D F Q K V P M O T G I L P G C E P C H K K V C A H G T C Q P S S H-Slit1

1339 E Q D F M D E - - - - - T P H I K E E P V D P C L E N K C R R G S R C V P N S D-Slit
1347 Q A G F T C E C Q E G W M G P L C D Q R T N D P C L G N K C V H G T - C L P I N H-Slit1

1373 N A R D G Y Q C K C K H G Q S R Y C D Q G E G S T E P - - - - - D-Slit
1386 A F - - S Y S C K C L E G H G G V L C D E E E D L F N P C Q A I K C K H G K C R H-Slit1

1401 - - - - - P T V T A A S - - - - - T C R K E Q V R E Y Y T E N D - D-Slit
1424 L S G L G Q P Y C E C S S G Y T G D S C D R E I S C R G E R I R D Y Y Q K Q Q G H-Slit1

1423 - - - C R S R Q P L K Y A K C V G G C - G N Q C C A A K I V R R R K V R M V C S D-Slit
1464 Y A A C Q T T K K V S R L E C R G G C A G G Q C C G P L R S K R R K Y S F E C T H-Slit1

1459 N N R K Y I K N L D I V R K C G C T K K C Y D-Slit
1504 D G S S F V D E V E K V V K C G C T R - C V S H-Slit1

007660" 54204560

TABLE 5(A)

Hybridisation Probes for regions of Human Slit-1

Hybridisation Probe for the first Leucine rich repeat region

TGCCCGGCGCAGTCTCTTGCTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCGCAGCGTGCCAGGAAT	75
ATCCCCGCAACACCGAGAGACTGGATTTAAATGGAATAACATCACAGAATTACGAAGACAGATTTTGCTGGT	150
CTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAAGAGGAGCATTCCAGGATCTT	225
AAAGAACTAGAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCTGAGTTGCTGTTTCTTGGGACTGCG	300
AAGCTATACAGGCTTGATCTCAGTGAACCAAAATTCAGGCAATCCCAAGGAAAGCTTTCCGTTGGGCGAGTTGAC	375
ATAAAAAATTTGCAACTGGATTACAACCAGATCAGCTGTATTGAAGATGGGGCATTTCAGGCTCTCCGGGACCTG	450
GAAGTGTCACTCTCAACAATAACAACATTACTAGACTTTCTGTGGCAAGTTTCAACCATATGCCTAAACTTAG	525
ACTTTTCGACTGCATTCAAACAACCTGTATTGTGACTGCCACCTGGCCTGGCTCTCCGACTGGCTTCGCAAAAGG	600
CCTCGGGTTGGTCTGTACACTCAGTGTATGGGCCCCCTCCACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAA	675
CGAGAATTGTCTCGAGTGATGAGGAAGAAGGTACCAGTCATTATGGCTCCTTCTGTAGTGTTTTGAC	747

82-828

Hybridisation Probe for the second Leucine rich repeat region

TGCCCTGCCGCTGTACCTGTAGCAACAATATCGTAGACTGTCGTGGGAAAGGTCTCACTGAGATCCCCACAAAT	75
CTTCCAGAGACCATCACAGAAATACGTTTGAACAGAACACAATCAAAGTCATCCCTCCTGGAGCTTTCTCACCA	150
TATAAAAGCTTAGACGAATTGACCTGAGCAATAATCAGATCTCTGAAGTTGACACAGATGCTTTCCAGGACTA	225
CGCTCTCTGAATCACTTGTCTCTATGGAATAAAATCACAACTCCCCAAAGTTTATTGAAGGACTGTTT	300
TCCTTACAGCTCCTATTATTGAATGCCAACAGATAAACTGCCCTTCGGGTAGATGCTTTTCAGGATCTCCACAAC	375
TGAACCTTCTCTCCCTATATGACAACAAGCTTCAGACCATCGCCAAGGGGACCTTTTCACTCTTCGGGCCATT	450
CAAACTATGCATTGGCCCGAAGCCCTTTTATTTGTGACTGCCATCTCAAGTGGCTAGCGGATTATCTCCATACC	525
AACCCGATTGAGACAGTGGTGGCCGTTGCAAGCCCGCCGCTGGCAACAAAAGAATTGGACAGATCAAA	600
AGCAAGAAATTCGGTTGTTCAAGTACAGAAGATTATCGATCAAAATTAAGTGGAGACTGCTTTGCGGATCTGGCT	675

829-1503

Hybridisation Probe for the third Leucine rich repeat region

TGCCCTGAAAAGTGTGCTGTGAAGGAACCAAGTGAATTTGCTCTAATCAAAAGCTCAACAAAATCCCGGAGCAC	75
ATTCCCCAGTACACTGCAGAGTTGCGTCTCAATAATAATGAATTTACCGTGTGGAAGCCACAGGAATCTTTAAG	150
AAACTTCCTCAATTACGTAAATAAACTTTAGCAACAATAAGATCACAGATATTGAGGAGGGAGCATTGGAAGGA	225
GCATCTGGTGTAATGAAATACTTCTTACGAGTAATCGTTTGGAAAATGTGCAGCATAAGATGTTCAAGGGATTG	300
GAAAGCCTCAAACTTTGATGTTGAGAAGCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGT	375
TCTGTGCGTTTGTCTTTTGTATGATAATCAAAATTACTACAGTTGCACCAGGGGCATTGATACTCTCCATTCT	450
TTATCTACTCTAAACCTCTTGGCZAATCCTTTTAACTGTAAGTGTACCTGGCTTGGTTGGGAGAGTGGCTGAGA	525
AAGAAGAGAATTGTACGGGGAATCCTAGATGTCAAAACCATACTTCCTGAAAGAAATACCCATCCAGGATGTG	600
GCCATTCAAGACTTCACTTGTGATGACGGAATGATGACAATAGTTGCTCCCCACTTTCTCGC	663

1504-2106

Hybridisation Probe for the fourth Leucine rich repeat region

GTCTACTGAATGTAATTGCTTGGATACAGTCCGATGTAGCAACAAGGGTTTGAAGGTCTTGCCGAAAGGT	75
ATTCCAAGAGATGTCACAGAGTTGTATCTGGATGGAACCAATTTACACTGGTTCCCAAGGAATCTCCAATAC	150
AAACATTTAACACTTATAGACTTAAGTAACAACAGAATAAGCACGCTTCTAATCAGAGCTTCAGCAACATGACC	225
CAGCTCCTCACCTTAATCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCGCACCTTTGATGGATTAAAGTCT	300
CTTCGATTACTTTCTCTACATGGAATGACATTTCTGTTGTGCTGAAGGTGCTTTCAATGATCTTTCTGCATTA	375
TCACATCTAGCAATTGGAGCCAACCTCTTTACTGTGATTGTAACATGCAGTGGTTATCCGACTGGGTGAAGTCG	450
GAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCCCTGGAGAAATGGCAGATAAACTTTTACTCACAACCTCC	525
TCCAAAAAATTACCTGTCAAGGTCTGTGGATGTCAATATTCTAGCTAAGTGTAAACCC	585

2167-2751

Hybridisation Probe for EGF repeats one to five

TGCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTGATCCAGTTGACTTTTACCGATGCACCTGTCCA	75
TATGGTTTCAAGGGGCGAGACTGTGATGTCCCAATTCATGCTGCATCAGTAACCATGTAAACATGGAGGAAT	150
TGCCACTTAAAGGAAGGAGAAGAAGATGGATTCTGGTGTATTGTGCTGATGGATTTGAAGGAGAAAATTGTGA	225
GTCAACGTTGATGATTGTGAAGATAATGACTGTGAAAATAATTCTACATGTGTCGATGGCATTAAATACTACACA	300
TGCTTTGGCCACCTGAGTATACAGGTGAGTTGTGTGAGGAGAAGCTGGACTTCTGTGCCAGGACCTGAACCCC	375
TGCCAGCAGATTCAAAGTACATCCTAATCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAA	450
CACTGCGACATCGATTTTACGACTGCCAAGACAACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAAC	525
GGCTATACGTGCATATGCCCCGAAGGTTACAGTGGCTTGTCTGTGAGTTT	576

2752-3224

007630 5440550

TABLE 5(B)

Hybridisation Probe for the sixth EGF repeat and preceding spacer region

TCTCCACCCATGGTCTCCCTCGTACCAGCCCTGTGATAATTTTGATTGTCAGAATGGAGCTCAGTGATCGTC 75
AGAATAAATGAGCCAATATGTCAGTGTTTGCTGGCTATCAGGGAGAAAAGTGTGAAA 134

3028-3161

Hybridisation Probe for the 99aa spacer/G-loop region

ATTGGTTAGTGTGAATTTTATAACAAAGAGTCTTATCTTCAGATTCTTCAGCCAAGGTTCCGGCCTCAGACGAA 75
CATAACACTTCAGATTGCCACAGATGAAGACAGCGGAATCCTCCTGTATAAGGTTGACAAAGACCATATCGCGGT 150
AGAACTCTATCGGGGGCGTGTTCGTGCCAGCTATGACACCGGCTCTCATCCAGCTTCTGCCATTTACAGTGTGGA 225
GACAATCAATGATGGAACTTCCACATTGTGGAATACTTGCCTTGGATCAGAGTCTCTCTTTGTCCGTGGATGG 300
TGGGAACCCCAAATCATCACTAACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTCTATGTAGGAGG 375
CATGCCAGGGAAGAGTAACGTGGCATCTCTGCCCCAGGCCCTGGGCAGAACGGAACAGCTTCCACGGCTGCAT 450
CCGGAACCTTTACATCAACAGTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAACAGGCATTTTGCCTGGCTGT 526

3162-3987

Hybridisation Probe for EGF repeats seven to nine

GAGCCATGCCACAAGAAGGTGTGTGCCCATGGCAATGCCAGCCAGCAGCCAGGCAGGCTTCACCTGCGAGTGC 75
CAGGAAGGATGGATGGGGCCCTCTGTGACCAACCGACCAATGACCCTTGCTTGGAAATAAATGCGTACATGGC 150
ACCTGCTTGCCCATCAATGCGTTCTCCTACAGCTGTAACTGCTTGGAGGGCCATGGAGGTGTCTCTGTGATGAA 225
GAGGAGGATCTGTTTAACCCATGCCAGGCGATCAAGTCAAGCATGGGAAGTGCAGGCTTTCAGGTCTGGGGCAG 300
CCCTACTGTGAATGCAGCAGTGGATACACGGGGACACTGTGATCGAGAAATC 353

3988-4341

Hybridisation Probe for the cysteine knot region

TCTTGTCGAGGGGAAAGGATAAGAGATTATTCCTAAAGCAGCAGGGCTATGCTGCTTGCCAAACAACCAAGAAG 75
GTGTCCCGATTAGAGTGCAGAGGTGGGTGTGACGAGGGCAGTGCTGTGGACCGCTGAGGAGCAAGCGCGGAAA 150
TACTCTTTCGAATGCACTGACGGCTCTCTTGTGGACGAGGTTGAGAAAGTGGTGAAGTCCGGCTGTACGAGG 225
TGTGTGTCC 234

4342-4575

007660" 54304560

PCR Primers for regions of Human Slit-1

PCR Primers for the first Leucine rich repeat region

Forward: 5' TGCCCGGCGCAGTGCTCTTGCTCGGGCAGC 3' 82-111
 Reverse: 5' GTGCAAACTACTACAAGAAGGAGCCATAAA 3' 799-120 (82)

PCR Primers for the second Leucine rich repeat region

Forward: 5' TGCCCTGCCGCTGTACCTGTAGCAACAAT 3' 824-858
 Reverse: 5' AGCCAGATCCGCAAAGCAGTCTCCACTTAA 3' 1174-1572 RL

PCR Primers for the third Leucine rich repeat region

Forward: 5' TGCCCTGAAAAGTGTGCTGTGAAGGAACC 3' 1504-1533
 Reverse: 5' GCGAGAAAGTGGGAGCAACTATTGTCATC 3' 2137-2166

PCR Primers for the fourth Leucine rich repeat region

Forward: 5' TGTCTACTGAATGTACTTCTGGATACA 3' 2167-2196
 Reverse: 5' GGGTTACACTTAGCTAGAAATTGACATC 3' 2722-2751

PCR Primers for EGF repeats one to five

Forward: 5' TGCCTATCAAATCCGTGTAAAAATGATGGC 3' 2752-2781
 Reverse: 5' AAATCACAGAACAGCCACTGTAACCTTC 3' 3248-3327

PCR Primers for the sixth EGF repeat and preceding spacer region

Forward: 5' TCTCCACCCATGGTCCCTCCCTCGTACCAGC 3' 3329-3357
 Reverse: 5' TTTTCACACTTTTCTCCCTGATAGCCAGGC 3' 3432-3461

PCR Primers for the 99aa spacer/G-loop region

Forward: 5' ATTGGTTAGTGTGAATTTTATAAACAAAGA 3' 3462-3491
 Reverse: 5' ACAGCCAGGCAAAATGCCTGTTTGCATCGG 3' 3758-3787

PCR Primers for EGF repeats seven to nine

Forward: 5' GAGCCATGCCACAAGAAGGTGTGTGCCCAT 3' 3988-4017
 Reverse: 5' GATTTCTCGATCACAGCTGTCCCGTGTAT 3' 4312-4341

PCR Primers for the cysteine knot region

Forward: 5' TCTTGTCGAGGGGAAAGGATAAGAGATTAT 3' 4712-4731
 Reverse: 5' GGACACACCTCGTACAGCCGCACTTCAC 3' 4546-4575

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